

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.

(ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

(iii) NUMBER OF SEQUENCES: 11

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(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 460 Point San Bruno Blvd
- (C) CITY: South San Francisco
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 94080

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

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(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 31-Mar-1997
- (C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Marschang, Diane L.
- (B) REGISTRATION NUMBER: 35,600
- (C) REFERENCE/DOCKET NUMBER: P1007R1

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids
(B) TYPE: Amino Acid
10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
15 1 5 10 15

Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
20 20 25 30

Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
20 35 40 45

Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
25 50 55 60

Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
30 65 70 75

Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
30 80 85 90

Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
35 95 100 105

Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly

110 115 120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro
125 130 135

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Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His
140 145 150

10 Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys
155 160 165

Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro
170 175 180

15 Thr
181

(2) INFORMATION FOR SEQ ID NO:2:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGCTGGGGG CCCGGGCCAG NGGCAGCACT CGTAGCCCCA GGTGTGACTG 50

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TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTGTTGC AGAGGCTGCC 100

CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150

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ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACACCCA 200

TAATTCTGAA TGTGCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250

TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300

5 CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTCA 350

CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400

ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CCCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 1438 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50

TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100

15 AGCTCTATCC TGTGCCCTG GTGCGAGCAG GCAGCCCAGC GCTTCGCGTG 150

TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200

20 CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCCCGCCTCC 250

CCCCGCCCGC CAGGCGGGCC CTTCTCGACG GCGCGGGCGG GGCCCTGCGG 300

GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350

25 AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400

GCGGCGGTGG CGGCGGGCGCT CCTCCTGGTG CTGCTGGGG CCCGGGCCA 450

30 GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500

AGATTGGTCT GTTTGTTGC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550

35 GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600

AGACACCTTC TTGGCCTGGG AGAACCCACCA TAATTCTGAA TGTGCCCGCT 650

GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700

5 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750

CCAGGTCAAG CAATGTGTCA GCAGTTCACCC CTTCTACTGC CAACCATGCC 800

TAGACTGCCG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850

10 GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900

CTGCGTGTCC TGCCCCACGT AATTCTTAGC TGTCGTGGGA TGGAGGGAAG 950

15 GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000

CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050

GTGGGCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100

20 GCCTTAGCCA GATACATAAG GGTATTGCC TTCACTTCA GCCAGCATTC 1150

CCCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200

25 GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250

CAGTGAGCTA TGATCGTGCC ACTGCACCTTC AGCCTGGCA ACAGAGCGAG 1300

ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350

30 AATCTATTAA ATAAATAAAT ACAAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400

TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438

35 (2) INFORMATION FOR SEQ ID NO:6:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
1 5 10 15

Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
10 20 25 30

Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
15 35 40 45

Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
20 50 55 60

Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
25 65 70 75

Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
30 80 85 90

Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
25 95 100 105

Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly
30 110 115 120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro
35 125 130 135

Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His

140 145 150

Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys
155 160 165

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Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro
170 175 180

10 Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys
185 190 195

Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu
200 205 210

15 Val Val Pro Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg
215 220 225

His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly
230 235 240

20 Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu
245 250 255

25 Asp Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys
260 265 270

Ile Cys Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr
275 280 285

30 Pro Glu Thr Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp
290 295 300

Asp Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr
305 310 315

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Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met Met Leu Gln
320 325 330

5 Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val Pro Ala Arg
335 340 345

Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala Glu
350 355 360

10 Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln
365 370 375

Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Pro Ala Gly Leu
380 385 390

15 Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
395 400 405

20 Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
410 415 417

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAACGCC 27

35 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10 TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1634 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20 CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACACCGACG GGCAGAGAGC 50

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ACGGAGCCGG GAAGCCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94
Met Glu

1

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CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133
Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Leu

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CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr

20

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CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211
Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys
30 35 40

5 AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250
Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly
45 50

10 CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289
His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn
55 60 65

15 TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328
Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
70 75 80

20 TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367
Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln
85 90

25 GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406
Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu Asn
95 100 105

30 TGT TCA GCA GTG GCC GAC ACC CGC TGT GGC TGT AAG CCA 445
Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro
110 115

35 GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA TGT GTC AGC 484
Gly Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser
120 125 130

40 AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 523
Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly
135 140 145

GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA 562
Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg
150 155

5 GAT ACT GAC TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA 601
Asp Thr Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu
160 165 170

10 CAT GGC GAT GGC TGC GTG TCC TGC CCC ACG AGC ACC CTG 640
His Gly Asp Gly Cys Val Ser Cys Pro Thr Ser Thr Leu
175 180

15 GGG AGC TGT CCA GAG CGC TGT GCC GCT GTC TGT GGC TGG 679
Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys Gly Trp
185 190 195

20 AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT GGC CTT 718
Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu
200 205 210

25 GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA 757
Val Val Pro Leu Leu Gly Ala Thr Leu Thr Tyr Thr
215 220

30 TAC CGC CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA 796
Tyr Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala
225 230 235

35 GAT GAA GCT GGG ATG GAG GCT CTG ACC CCA CCA CCG GCC 835
Asp Glu Ala Gly Met Glu Ala Leu Thr Pro Pro Pro Ala
240 245

ACC CAT CTG TCA CCC TTG GAC AGC GCC CAC ACC CTT CTA 874
Thr His Leu Ser Pro Leu Asp Ser Ala His Thr Leu Leu
250 255 260

GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG 913
Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln
265 270 275

5 TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC 952
Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
280 285

10 CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC 991
Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp
290 295 300

CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC 1030
Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro
15 305 310

ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG 1069
Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met
315 320 325

20 ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC 1108
Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp
330 335 340

25 GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG 1147
Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr
345 350

30 CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG 1186
Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val
355 360 365

GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC 1225
Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu
35 370 375

AAG CGC TGG CGC CAG CAG CAG CCC GCG GGC CTC GGA GCC 1264
Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala
380 385 390

5 GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303
Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
395 400 405

10 GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340
Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
410 415 417

GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAGC 1390

15 CCTAAGTACG GTTACTTATG CGTAGACA TTTTATGTCA CTTATTAAGC 1440

CGCTGGCACG GCCCTGCGTA GCAGCACCAAG CCGGCCAAC CCCTGCTCGC 1490

CCCTATCGCT CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG 1540

20 GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGGTA 1590

TTAAATCTGT GAAAGAAAAC AAAAAAAA AAAAAAAA AAAA 1634

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: Nucleic Acid
- 30 (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:11:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

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